

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/507,763
Source: TFWP
Date Processed by STIC: 2/27/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 02/27/2006

PATENT APPLICATION: US/10/567,763

TIME: 14:42:07

Input Set : A:\21864wo.ST25.txt

Output Set: N:\CRF4\02272006\J567763.raw

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3 <110> APPLICANT: DSM IP Assets B.V.
5 <120> TITLE OF INVENTION: Microbial production of L-ascorbic acid
7 <130> FILE REFERENCE: 21864 WO
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/567,763
C--> 9 <141> CURRENT FILING DATE: 2006-02-10
9 <150> PRIOR APPLICATION NUMBER: EP 03017677.0
10 <151> PRIOR FILING DATE: 2003-08-14
12 <160> NUMBER OF SEQ ID NOS: 31
14 <170> SOFTWARE: PatentIn version 3.2
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2367
18 <212> TYPE: DNA
19 <213> ORGANISM: Gluconobacter oxydans N44-1
21 <400> SEQUENCE: 1
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24 gccttcctga tcatcgagg cctccacctc atcatcctcg gcggtcctg gttctacacc      120
26 ctgcgccgca tcgcgctggc ggccagcagc gtctacatga tccgtcgcaa cctcctctcg      180
28 acatggatcg ccctgggcct gcttgtggca acagccctgt ggtcgctcgc cgaagtcggc      240
30 accagcttct ggcccagctt ctcccgcctg atcgtgttcc tgtgcgtcgc cctgatcgcg      300
32 actctcatgg cgccctggct cagcggcccc ggccggcgct acttcacccg ccccgtcaca      360
34 ggcgccacat ccggcgccct cggcgcgatc atcgtggctt tcctcgccgg catgttccgg      420
36 gtccacccca ccacgcccc gcaggacacc acccaccgc aggaaaccgc gtccaccgcc      480
38 gactccgacc agccaggcca tgactggccc gcctatggcc gcacggcttc cggcacgcgc      540
40 tacgccagct tcacgcagat caaccgcgac aatgtcagca agctccgct cgccctggacc      600
42 taccgcaccg gcgacatggc gctgaacggc gccgagttcc agggcacccc catcaagatc      660
44 ggcgacacgg tctatatctg ctaccgcac aacatcgtct cggcccttga cccggacacc      720
46 ggcacggaaa agtggaagtt cgacccccac gccagacga aagtctggca gcgctgccgc      780
48 ggcgtcggct actggcatga cagcacggcc acggacgcca acgcgccctg cgctcgcgc      840
50 atcgtcctca ccacgatcga cgcccgctc atcaccatcg acgcccgtac cggccaggcc      900
52 tgcacggatt tcggaacgaa cggcaacgtc aatctcctga ccggcctcgg cccgacagct      960
54 cccggctcgt actaccgac cgccgcccc ctcgtggcgg gtgacatcgt ggtcgtcggc      1020
56 ggcgcacatg ccgataacga gcgcaccggc gagccctccg gcgtcgtccg cggctatgat      1080
58 gtccgcaccg gcgcacaggt ctgggcctgg gagccacca acccgcatcg cggcaccaca      1140
60 cctctggccg aaggcgagat ctaccccgcc gaaaccccca acatgtgggg caccgccagc      1200
62 tacgaccgga aactcaacct cgtcttcttc ccgctcggca accagacccc cgatttcttg      1260
64 ggcggcgacc gcagcaaggc ctacagacga tacaacgacg ccttcgtcgc cgtggacgcc      1320
66 aagaccggcg acgaacgctg gcacttcgc accgccaacc acgacctcgt ggactacgat      1380
68 gccacggccc agcccatcct ctatgacatt ccggacggcc atggcggcac ccgcccggcg      1440
70 atcatcgcca tgaccaagcg cggccagatc ttctgtctcg accgcgcga cggcaccgac      1500
72 atcgtccctg tggaaatcg caaagtcctc caggacggcg caccggaaca ccagtacctc      1560
74 gcccgaac agccctattc cgccctctcc atcggaacag agcgctgaa acccagcgac      1620
76 atgtggggtg gtacgatctt cgaccagctc ctgtgccgca tccagttcgc ctctaccgc      1680
78 tatgaaggcg agttcacccc cgtcaacgag aaacaggcca ccatcatcta tccgggctat      1740

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80 tacggcgcca tcaactgggg cggcggcgcc gtggatgaaa gcaccggaac gctgctggtc 1800
82 aacgacatcc gcatggccca gtggggcaag ttcataagc aggaagaagc ccgtcgagc 1860
84 ggcttcaaac ccagctcgga aggcgaatat tccgaacaga aaggcaccac ctggggcgctc 1920
86 gtccgctcga tgttcttctc ccccgccggt ctccctgcg tgaaaccgcc ctatggcacg 1980
88 atgaacgcca tcgacctgcg cagcggcaag gtcaaataga gcatgccgct tggcacgac 2040
90 caggacatgc cgggtccacg catggtccca ggccctcgca tcccgctcgg aatgccgacc 2100
92 atgagcggcc cgctggccac ccataccggc ctggtgttct tctccggcac gctcgacaac 2160
94 tatgtccgcg cgctcaacac cgacaccggc gaagtcgtct ggaaagcccg tctccccgctc 2220
96 gcctcacagg ccgctccgat gagctacatg tccgacaaga ccggcaaaca gtacatcgctc 2280
98 gtcaccgcag gcggcctgac ccgctccggc gtcgacaaaa accgcggcga ctacgtcatc 2340
100 gcctacgccc tgccctccga agaataa 2367
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 788
105 <212> TYPE: PRT
106 <213> ORGANISM: Gluconobacter oxydans N44-1
108 <400> SEQUENCE: 2
110 Met Asn Ser Gly Pro Arg Thr Leu Ser Met Ile Ile Gly Ile Leu Gly
111 1 5 10 15
114 Ala Leu Met Ala Ala Phe Leu Ile Ile Glu Gly Leu His Leu Ile Ile
115 20 25 30
118 Leu Gly Gly Ser Trp Phe Tyr Thr Leu Ala Gly Ile Ala Leu Ala Ala
119 35 40 45
122 Ser Ser Val Tyr Met Ile Arg Arg Asn Ile Leu Ser Thr Trp Ile Ala
123 50 55 60
126 Leu Gly Leu Leu Val Ala Thr Ala Leu Trp Ser Leu Ala Glu Val Gly
127 65 70 75 80
130 Thr Ser Phe Trp Pro Ser Phe Ser Arg Leu Ile Val Phe Leu Cys Val
131 85 90 95
134 Ala Leu Ile Ala Thr Leu Met Ala Pro Trp Leu Ser Gly Pro Gly Arg
135 100 105 110
138 Arg Tyr Phe Thr Arg Pro Val Thr Gly Ala Thr Ser Gly Ala Leu Gly
139 115 120 125
142 Ala Ile Ile Val Ala Phe Leu Ala Gly Met Phe Arg Val His Pro Thr
143 130 135 140
146 Ile Ala Pro Gln Asp Thr Thr His Pro Gln Glu Thr Ala Ser Thr Ala
147 145 150 155 160
150 Asp Ser Asp Gln Pro Gly His Asp Trp Pro Ala Tyr Gly Arg Thr Ala
151 165 170 175
154 Ser Gly Thr Arg Tyr Ala Ser Phe Thr Gln Ile Asn Arg Asp Asn Val
155 180 185 190
158 Ser Lys Leu Arg Val Ala Trp Thr Tyr Arg Thr Gly Asp Met Ala Leu
159 195 200 205
162 Asn Gly Ala Glu Phe Gln Gly Thr Pro Ile Lys Ile Gly Asp Thr Val
163 210 215 220
166 Tyr Ile Cys Ser Pro His Asn Ile Val Ser Ala Leu Asp Pro Asp Thr
167 225 230 235 240
170 Gly Thr Glu Lys Trp Lys Phe Asp Pro His Ala Gln Thr Lys Val Trp
171 245 250 255
174 Gln Arg Cys Arg Gly Val Gly Tyr Trp His Asp Ser Thr Ala Thr Asp

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175          260          265          270
178 Ala Asn Ala Pro Cys Ala Ser Arg Ile Val Leu Thr Thr Ile Asp Ala
179          275          280          285
182 Arg Leu Ile Thr Ile Asp Ala Arg Thr Gly Gln Ala Cys Thr Asp Phe
183          290          295          300
186 Gly Thr Asn Gly Asn Val Asn Leu Leu Thr Gly Leu Gly Pro Thr Ala
187 305          310          315          320
190 Pro Gly Ser Tyr Tyr Pro Thr Ala Ala Pro Leu Val Ala Gly Asp Ile
191          325          330          335
194 Val Val Val Gly Gly Arg Ile Ala Asp Asn Glu Arg Thr Gly Glu Pro
195          340          345          350
198 Ser Gly Val Val Arg Gly Tyr Asp Val Arg Thr Gly Ala Gln Val Trp
199          355          360          365
202 Ala Trp Asp Ala Thr Asn Pro His Arg Gly Thr Thr Pro Leu Ala Glu
203          370          375          380
206 Gly Glu Ile Tyr Pro Ala Glu Thr Pro Asn Met Trp Gly Thr Ala Ser
207 385          390          395          400
210 Tyr Asp Pro Lys Leu Asn Leu Val Phe Phe Pro Leu Gly Asn Gln Thr
211          405          410          415
214 Pro Asp Phe Trp Gly Gly Asp Arg Ser Lys Ala Ser Asp Glu Tyr Asn
215          420          425          430
218 Asp Ala Phe Val Ala Val Asp Ala Lys Thr Gly Asp Glu Arg Trp His
219          435          440          445
222 Phe Arg Thr Ala Asn His Asp Leu Val Asp Tyr Asp Ala Thr Ala Gln
223          450          455          460
226 Pro Ile Leu Tyr Asp Ile Pro Asp Gly His Gly Gly Thr Arg Pro Ala
227 465          470          475          480
230 Ile Ile Ala Met Thr Lys Arg Gly Gln Ile Phe Val Leu Asp Arg Arg
231          485          490          495
234 Asp Gly Thr Pro Ile Val Pro Val Glu Met Arg Lys Val Pro Gln Asp
235          500          505          510
238 Gly Ala Pro Glu His Gln Tyr Leu Ala Pro Glu Gln Pro Tyr Ser Ala
239          515          520          525
242 Leu Ser Ile Gly Thr Glu Arg Leu Lys Pro Ser Asp Met Trp Gly Gly
243          530          535          540
246 Thr Ile Phe Asp Gln Leu Leu Cys Arg Ile Gln Phe Ala Ser Tyr Arg
247 545          550          555          560
250 Tyr Glu Gly Glu Phe Thr Pro Val Asn Glu Lys Gln Ala Thr Ile Ile
251          565          570          575
254 Tyr Pro Gly Tyr Tyr Gly Gly Ile Asn Trp Gly Gly Gly Ala Val Asp
255          580          585          590
258 Glu Ser Thr Gly Thr Leu Leu Val Asn Asp Ile Arg Met Ala Gln Trp
259          595          600          605
262 Gly Lys Phe Met Lys Gln Glu Glu Ala Arg Arg Ser Gly Phe Lys Pro
263          610          615          620
266 Ser Ser Glu Gly Glu Tyr Ser Glu Gln Lys Gly Thr Pro Trp Gly Val
267 625          630          635          640
270 Val Arg Ser Met Phe Phe Ser Pro Ala Gly Leu Pro Cys Val Lys Pro
271          645          650          655

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274 Pro Tyr Gly Thr Met Asn Ala Ile Asp Leu Arg Ser Gly Lys Val Lys
 275 660 665 670
 278 Trp Ser Met Pro Leu Gly Thr Ile Gln Asp Met Pro Val His Gly Met
 279 675 680 685
 282 Val Pro Gly Leu Ala Ile Pro Leu Gly Met Pro Thr Met Ser Gly Pro
 283 690 695 700
 286 Leu Ala Thr His Thr Gly Leu Val Phe Phe Ser Gly Thr Leu Asp Asn
 287 705 710 715 720
 290 Tyr Val Arg Ala Leu Asn Thr Asp Thr Gly Glu Val Val Trp Lys Ala
 291 725 730 735
 294 Arg Leu Pro Val Ala Ser Gln Ala Ala Pro Met Ser Tyr Met Ser Asp
 295 740 745 750
 298 Lys Thr Gly Lys Gln Tyr Ile Val Val Thr Ala Gly Gly Leu Thr Arg
 299 755 760 765
 302 Ser Gly Val Asp Lys Asn Arg Gly Asp Tyr Val Ile Ala Tyr Ala Leu
 303 770 775 780
 306 Pro Ser Glu Glu
 307 785

310 <210> SEQ ID NO: 3

311 <211> LENGTH: 20

312 <212> TYPE: DNA

313 <213> ORGANISM: Artificial

315 <220> FEATURE:

316 <223> OTHER INFORMATION: Primer

318 <400> SEQUENCE: 3

319 cgccttctat gaaagggttg

20

322 <210> SEQ ID NO: 4

323 <211> LENGTH: 20

324 <212> TYPE: DNA

325 <213> ORGANISM: Artificial

327 <220> FEATURE:

328 <223> OTHER INFORMATION: Primer

330 <400> SEQUENCE: 4

331 agcggatgga gatcgggcgg

20

334 <210> SEQ ID NO: 5

335 <211> LENGTH: 30

336 <212> TYPE: DNA

337 <213> ORGANISM: Artificial

339 <220> FEATURE:

340 <223> OTHER INFORMATION: Primer

342 <400> SEQUENCE: 5

343 atgaacagcg gccccgcac gctctccatg

30

346 <210> SEQ ID NO: 6

347 <211> LENGTH: 30

348 <212> TYPE: DNA

349 <213> ORGANISM: Artificial

351 <220> FEATURE:

352 <223> OTHER INFORMATION: Primer

354 <400> SEQUENCE: 6

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355 ccggaacatg ccggcgagga aagccacgat      30
358 <210> SEQ ID NO: 7
359 <211> LENGTH: 30
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial
363 <220> FEATURE:
364 <223> OTHER INFORMATION: Primer
366 <400> SEQUENCE: 7
367 tgactggccc gcctatggcc gcacggcttc      30
370 <210> SEQ ID NO: 8
371 <211> LENGTH: 30
372 <212> TYPE: DNA
373 <213> ORGANISM: Artificial
375 <220> FEATURE:
376 <223> OTHER INFORMATION: Primer
378 <400> SEQUENCE: 8
379 ttcttcggag ggcaggcgt aggcgatgac      30
382 <210> SEQ ID NO: 9
383 <211> LENGTH: 30
384 <212> TYPE: DNA
385 <213> ORGANISM: Artificial
387 <220> FEATURE:
388 <223> OTHER INFORMATION: Primer
390 <400> SEQUENCE: 9
391 cgggactttg cgcatttcca cagggacgat      30
394 <210> SEQ ID NO: 10
395 <211> LENGTH: 30
396 <212> TYPE: DNA
397 <213> ORGANISM: Artificial
399 <220> FEATURE:
400 <223> OTHER INFORMATION: Primer
402 <400> SEQUENCE: 10
403 agcccatcct ctatgacatt ccggacggcc      30
406 <210> SEQ ID NO: 11
407 <211> LENGTH: 771
408 <212> TYPE: DNA
409 <213> ORGANISM: Gluconobacter oxydans IFO 3292
411 <400> SEQUENCE: 11
412 ccgcccggcg atcatcgcca tgaccaagcg cggccagatc ttcgtgctcg accgccgcga      60
414 cggcaccgcc atcgtccccc tggaaatgcg caaagtcccc caggacggcg caccggaaca      120
416 ccagtacctc gccccgaac agccctattc cgccctctcc atcggaacag agcgcttgaa      180
418 acccagcgat atgtggggcg gcacgatctt cgaccagctc ctgtgccgca tccagttcgc      240
420 ctccctaccgc tatgaaggcg agttcacccc cgtcaacgag aagcaggcca ccatcatcta      300
422 tccgggctat tacggcgggc tcaactgggg cggcgggcgc gtggatgaaa gcaccggaac      360
424 gctgctggtc aacgacatcc gcatggccca gtggggcaag ttcatgaagc aagaagaagc      420
426 ccgccgcagc ggcttcaaac ccagctcgga aggcgaatat tccgaacaga aaggcacccc      480
428 ctggggcgtc gtccgctega tgttcttctc ccccgccggt ctccctcgcg tgaaaccgcc      540
430 ctatggcacg atgaacgcca tcgacctgcg cagcggcaag gtcaaattgga gcatgccgct      600
432 tggcacgata caggacatgc cggctccacg catggtcccc ggctcgcga tcccgctcgg      660

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/567,763

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Input Set : A:\21864wo.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 123

Seq#:19; N Pos. 123

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,23,24,25,28,29,30,31

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/567,763

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Input Set : A:\21864wo.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:120

L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:120